

FIGURE 1

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTTCGATTTCTGTTGCCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGGAGCGGCCCGCGCTGCTGGGCGAGCGCAGGAGCGGGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCCGGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCGACGGCAGCGTGCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGAAGTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

Query:	170	TGGCGCACCTGACGGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC	229
Sbjct:	2	TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCACT	61
Query:	230	TGCAGATCCTGCCCCACGGCAGCGTGCCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTA	289
Sbjct:	62	TAGAAATCTTCCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTTGGCA	121
Query:	290	TCTTGAATTTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC	349
Sbjct:	122	TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTTCGAGGCGTGGACAGTGGAC	181
Query:	350	TCTATCTTGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCCGAAT	409
Sbjct:	182	TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT	241
Query:	410	GCATCTTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTTCATCTAACATATATA	469
Sbjct:	242	GTGTATTTCAGAGAACAGTTCGAAGAAACTGGTATAATACGTACTCGTCAAACCTATATA	301
Query:	470	AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCAAGAG	529
Sbjct:	302	AGCACGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG	361
Query:	530	ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC	589
Sbjct:	362	AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC	421
Query:	590	CAGA	593
Sbjct:	422	CCGA	425

FIGURE 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query:   289 TACCGAAGAGGCTGTGGTCCTGCCGCGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
          |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCCTGCCGCGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query:   229 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGGGCGCAGGATGCCGTGCAGGTGCGCCA 170
          |||
Sbjct: 15987 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGG-CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query:   169 GCTGCGCAGCCCCCGGCGCGCGCGCGGCGCTCCGCTCCGCGCGCGCTCCTGCGCTCGCCCA 110
          |||
Sbjct: 16046 GCTGCGCAGCCCCCGGCGCGCGCGCGGCGCTCCGCTCCGCGCGCGCTCCTGCGCTCGCCCA 16105

Query:   109 GCAGCGGCGGCGCGCTCCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGCGCCA 50
          |||
Sbjct: 16106 GCAGCGGCGGCGCGCTCCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGCGCCA 16165

Query:    49 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
          |||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query:   633 AGTGATACATCAGTAGGTCCTTGTAACAATTCTGGAACTCTTTCTGGATCCACTGGTCTAGG 574
          |||
Sbjct: 7257 AGTGATACATCAGTAGGTCCTTGTAACAATTCTGGAACTCTTTCTGGATCCACTGGTCTAGG 7316

Query:   573 TAAGAAATGTGTAAATTTCTGATGCTCTTGACCTGGCGCCATCTCTTGAGATTCCGTC 514
          |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCTCTTGACCTGGCGCCATCTCTTGAGATTCCGTC 7376

Query:   513 TTTGTAAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
          |||
Sbjct: 7377 TTTGTAAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query:   453 ATAGGTGTTATACCAATTCTCTTCAAACCTGCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 394
          |||
Sbjct: 7437 ATAGGTGTTATACCAATTCTCTTCAAACCTGCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 7496
```

FIGURE 3 (cont.)

Query: 393 CTC-TGATCCATAGA 380
 ||| ||| | |||
 Sbjct: 7497 CTCCTGAAAGAGAGA 7511

C.

Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
 Identities = 106/106 (100%), Positives = 106/106 (100%),
 Strand = Minus / Plus

Query: 391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

Query: 331 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 286
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 9897 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 9942

FIGURE 4

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGE-CX (EAA93474Xen; Xenopus laevis XFGE CX) [SEQ ID NO:12]
5. FGF-CX (CGA5020859) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

```

M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
M A P L A D V G T F L G G Y D A L G - Q V G S H F L L P P A K D S P L L F N D P L A Q S E R L S R - S A P - - S D L S H
M A P L A E V G G F L G G L E G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A E R S A R - G G P G A A Q L A H

L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L Q G I L R R R Q L Y C R T G F H L Q I L P D G N V Q G T R Q Q D H S R F G I L E F I S V A I G L V S I R G V D T G L Y L
L H G I L R R R Q L Y C R T G F H L Q I L P D G S V Q G T R Q Q D H S L F G I L E F I S V A V G L V S I R G V D S G L Y L

G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N D K G E L F G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R Y F V A L N K D G T P R D G T
G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N I Y K H G D T G R R Y F V A L N K D G T P R D G A

```

```

R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R A K R H Q K F T H F L P R P V D P D K V P E L Y K D L M G Y S
R S K R H Q K F T H F L P R P V D P D E R V P E L Y K D L L M Y T

```

FIGURE 5

FGF-CX	MAPLAEVGGFLGGLEGLGQVGSFHLLPPAGERPPLGERRSAAERSARGGPGAAQLAH	59
XFGF-20	MAPLADVGTFLGGYDALGQVGSFHLLPPAKDSPLFNDPLAQSERLSR-SAP--SDLSH	56
FGF-9	MAPLGEVGNVFGVQDAVP--FENVPLP--VDSVLLSDHLGQSEAGGLPREPAVTDLDH	56
FGF-CX ₁₆	--MAEVGGVFASLDWDLHGFSLSGNVPLADSPGFLNERLGQIEGKLQREGSP--TDFAH	55
FGF-20	LHGILRRRQLYCRTGTFHLQILPDGSVQGTRODHSLEFGILEFISVAVGLVSIRGVDSGLYL	119
XFGF-20	LQGI LRRRQLYCRTGTFHLQILPDGNWQGTRODHSRFGILEFISVALGLVSIRGVDTGLYL	116
FGF-9	LKGI LRRRQLYCRTGTFHLEIFPNGTQQGTREKDSRFGILEFISIAVGLVSIRGVDSGLYL	116
FGF-16	LKGI LRRRQLYCRTGTFHLEIFPNGTVHGTREHDSRFGILEFISIAVGLVSIRGVDSGLYL	115
FGF-20	GMNDKGLYGSSEKLTSECI FREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA	179
XFGF-20	GMNDKGLYGSSEKLTSECI FREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGT	176
FGF-9	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYFVALNKDGTPREGT	176
FGF-CX ₁₆	GMNERGELYGSKKLTREC VFREQFEENWYNTYASTLYKHSDSERQYFVALNKDGSPEEZY	175
FGF-20	RSKRHHQKFTHFLPRPVDPERWPELYKDLLMYT	211
XFGF-20	EAKRHHQKFTHFLPRPVDPEKVP ELYKDLLMGYS	208
FGF-9	R TKRHHQKFTHFLPRP VDPDKVPELYKDILSQS	208
FGF-16	R TKRHHQKFTHFLPRP VDPDKLPSMSRDLFHYR	207

FIGURE 6

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

```
Query:      1 MAPLAEVGGFLGLEGQQVGSFHLLPPACERPPDLLGERSSAAERSARG - GPGAQQLAH   59
          ||| | + | + + + + + + | + | + | | | + | | | |
Sbjct:     1 MAPLGEVGNFYGVQDAV--PFCNVPLPV--DSPVLSDHLGQSEAGGLPRGPAVTDLDH   56

Query:    60 LHGILRRRLYCRPTGFHLQILPDGVSQGTRDHSIFLGILEFISVAVGLSVIRGVDSGLYL   119
          | | | | | | | | | | | | | + | + + + + + + | | | | | | | | | |
Sbjct:    57 LKGILRRRLYCRPTGFHLEIFPNGTIQGTRKDHRSRFGILEFISIAVGLSVIRGVDSGLYL   116

Query:    120 GMNDKGELYGSEKLITSECIFREQFEENWNTYSNNIYKHGDTGRRYFVALNKDGTPRDGA   179
          || |+|||+|||||++|||||++++|||+|||||+|||||++|
Sbjct:    117 GMEKEGELYGSEKLITQECVFREQFEENWNITYSSNLYKHVDTGRRYYVALNKDGTREGT   176

Query:    180 RSKRHQKFTHFLRPVPDPERPVELYKDLL   208
          |+|||+|||||+++|||||+|
Sbjct:    177 RTKRHQKFTHFLRPVPDPDKVPELYKDIL   205
```

FIGURE 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```

Query:      1  MAPLAEVGGFTGLEGLGQQVGSFHLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH  59
          ||||| + | + + + | + + | + | + + | + | + | + | + |
Sbjct:      1  MAPLGEVGSYFGVQDAV--PFGNVPLPV--DSPVLLNDHLGQSEAGGLPRGPVATDLDH  56

Query:     60  LHGILRRRLQYCRGTGFHLQILPDGSVQGTQRQDHSFLFGILEFISVAVGLVSIRGVDSGLYL  119
          | ||||| ||||| ||||| + | + + ||||| + ||||| ||||| ||||| |||||
Sbjct:     57  LKGILRRRLQYCRGTGFHLEIFPNGTIQGTRKDHRSFRFGILEFISIAVGLVSIRGVDSGLYL  116

Query:     120  GMNDFKELYGSEKLTSECIFFREQFEENWINTYSSNIYKHGDTGRRIFVALNKDGTPRDGA  179
          |||+||||| ||||| + ||||| ||||| ||||| ||||| ||||| + |||||
Sbjct:     117  GMNEKGELYGSEKLTQECVFRQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGT  176

Query:     180  RSKRHQKFTFHLPRPVPDPERVPELYKDLL  208
          |+||||| ||||| ||||| + ||||| ||||| + |||||
Sbjct:     177  RTRKHQKFTFHLPRPVPDPDKVPELYKDIL  205

```


FIGURE 8

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
 Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:	1	MAPLAEVGGFLGGLGQVQVGSFHLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH	59
		+ + + + + + + +	
Sbjct:	1	MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH	56
Query:	60	LHGILRRRQLYCRITGFHLQILPDGSVQGTQRQDHSLSFGILEFISVAVGLVSIRGVDSGLYL	119
		+ + + +	
Sbjct:	57	LKGILRRRQLYCRITGFHLEIFPNGTIQGTRKDHRSRFGILEFISIAVGLVSIRGVDSGLYL	116
Query:	120	GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA	179
		+ + + +	
Sbjct:	117	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGT	176
Query:	180	RSKPHQKFTHFLPPVDPDPVPPELYKDIL	208
		+ + + +	
Sbjct:	177	RTKRHQKFTHFLPRPVDPKVPPELYKDIL	205

FIGURE 9

FGF-CX Query Length = 211
 XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
 Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

Query:	1	MAPLAEVGGFLGGLEGLGQQVGSFHLPPAGERPPLLGERPSAAERSAPGGPGAAQLAHL	60
		+ + + + + + +	
Sbjct:	1	MAPLADVGTFLGGYDALGQ-VGSFHLPPAKDSPLENDPLAQSERLSRSAP--SDLSHL	57
Query:	61	HGILRRRLYCRGTGFHLQILPDGVSQGTQDHSLFGILEFISVAVGLVSIPIGVDSGLYL	120
Sbjct:	58	QGILRRRLYCRGTGFHLQILPDGNVQGTQDHSRFGILEFISVAIGLVSIPIGVDTGLYL	117
Query:	121	MNDKGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR	180
		+	
Sbjct:	118	MNDKGELFGSEKLTSECIFREQFEENWNTYSSNLKYGDSGRRYFVALNKDGTPRDGR	177
Query:	181	SKRHQKFTHFLPRPVDPERVPELYKDLMYT	211
		+	
Sbjct:	178	AKRHQKFTHFLPRPVDPEKVPPELYKDLMGYS	208

FIGURE 10

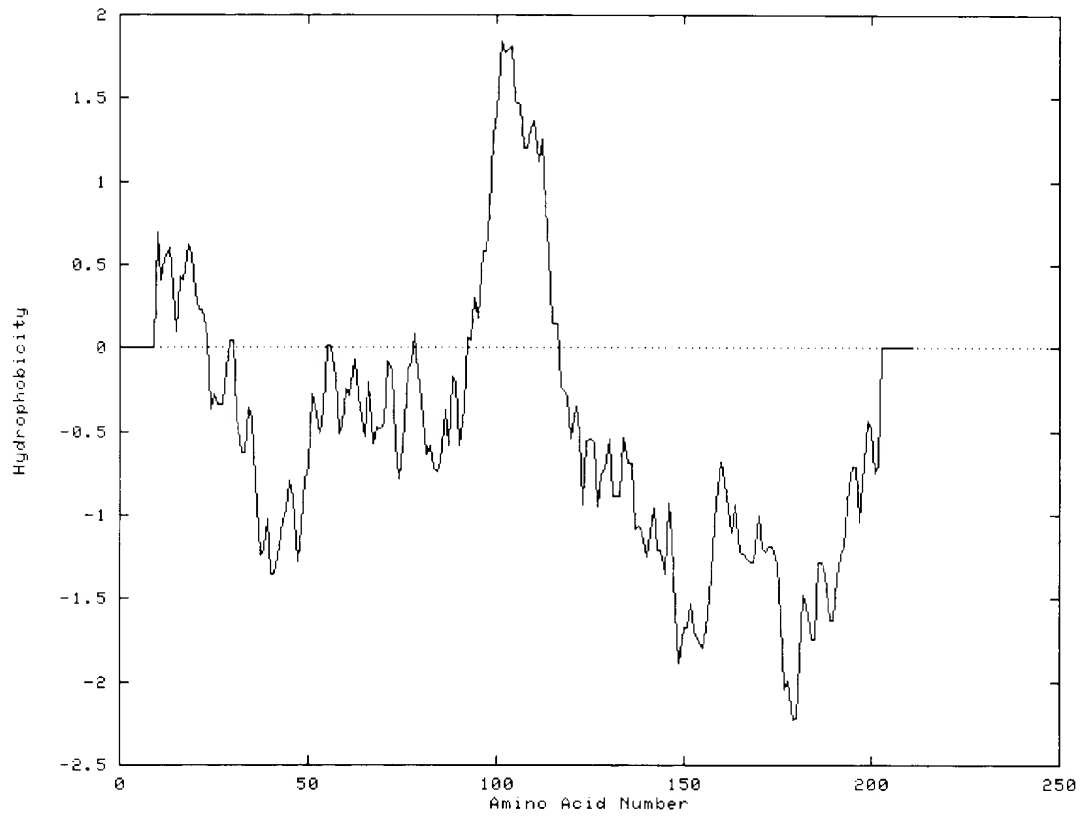
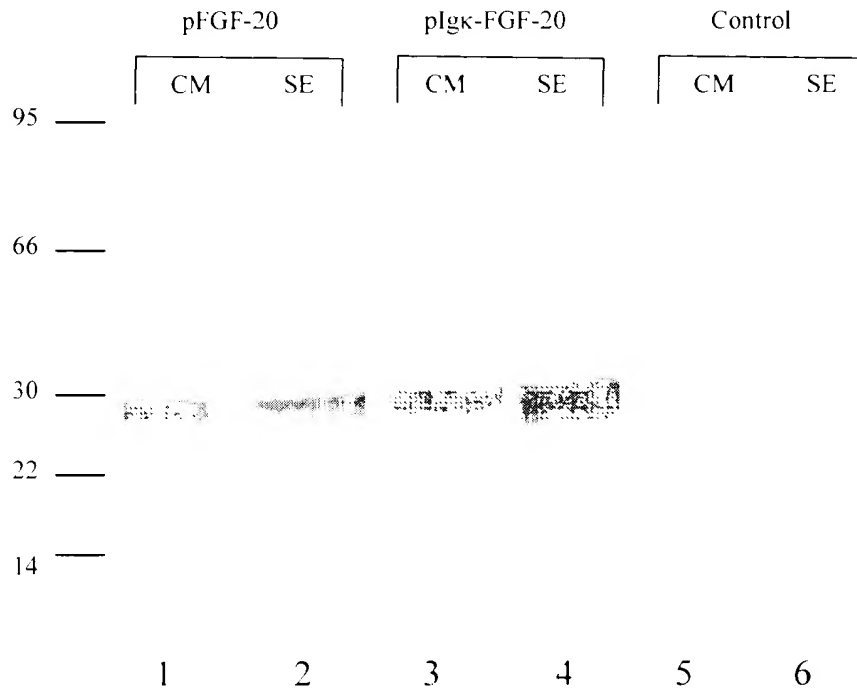


FIGURE 11

Panel A



Panel B

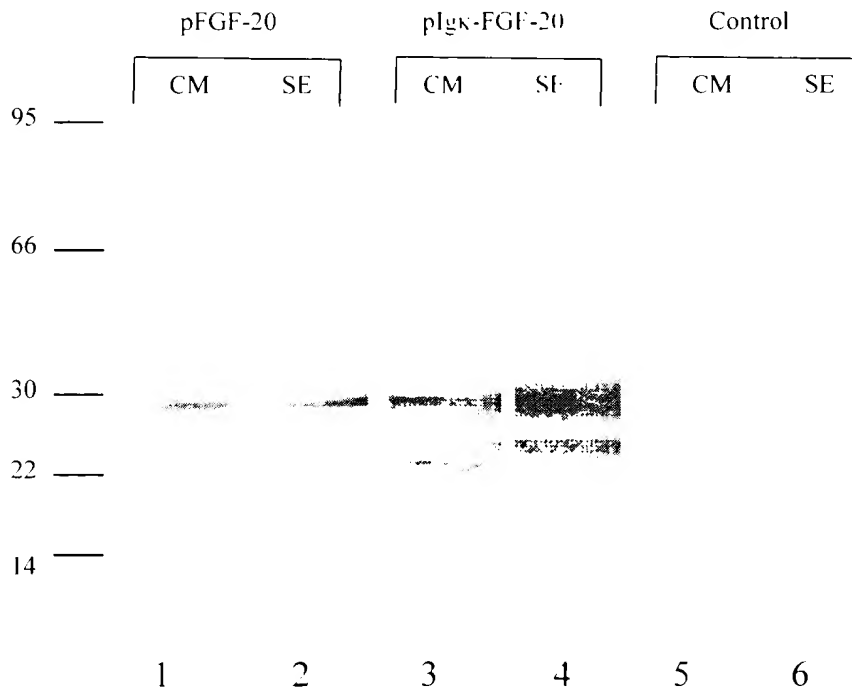


FIGURE 12.

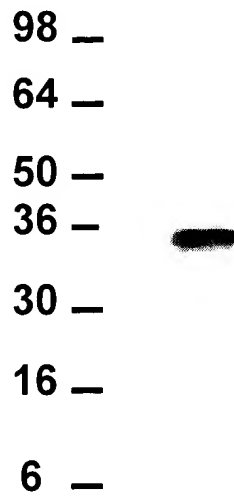


Figure 13.

Exon 1
...AGACAGTGAGAGCTTCCCTGCCCATTTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAAACCGGGCCTTAACT
TTTGGCGCTCGTTTGGCTATAAATTTTCTCTATCCACCTCCATCCACCCCAACAACACTCTTTACTGGGGGGTCTTTT
GTGTTCCGGATCTCCCCCTCC**ATGG**CTCCCTTAGCCGAAGTGGGGGCTTTCTGGCGGCTTGAGGGCTTGGGCCAGCA
M A P L A E V G G F L G G L E G L G Q Q
1
21 V G S H F L L P P A G E R P P L L G E R R S A A E R S
GGTGGGTTCGCATTTCCCTGTTCCTCCTGCCGGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGGAGCGGA
48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T
GGCGCGCGGGGGCTGGCGCAGCTGGCGCACCTGCACGGCATCCTGCGCCGCGCGCAGCTCTATTGCCGCACC
<-|-> **Exon 2**
74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F
GGTTCCACCTGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAGGACCCACAGCCTCTTCGGTATCTTGGAAAT
CATCAGTGTGGCAGTGGGACTGGTCACTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGAAATGAATGACAAAGGAGAAC
101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L
<-|-> **Exon 3**
TCTATGGATCAGAGAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCACT
128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S
AACATATATAAACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAAACAAAGACGGAACTCCAAGAGATGGCGCCAG
154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R
GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTTCAGAAATTTGTACAAGGACC
181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L
TACTGATGTACACT**TGA**...
208 L M Y T

Figure 14.

98_

64_

50_

36_

30_

16_

6 _

Figure 15, Panel A.

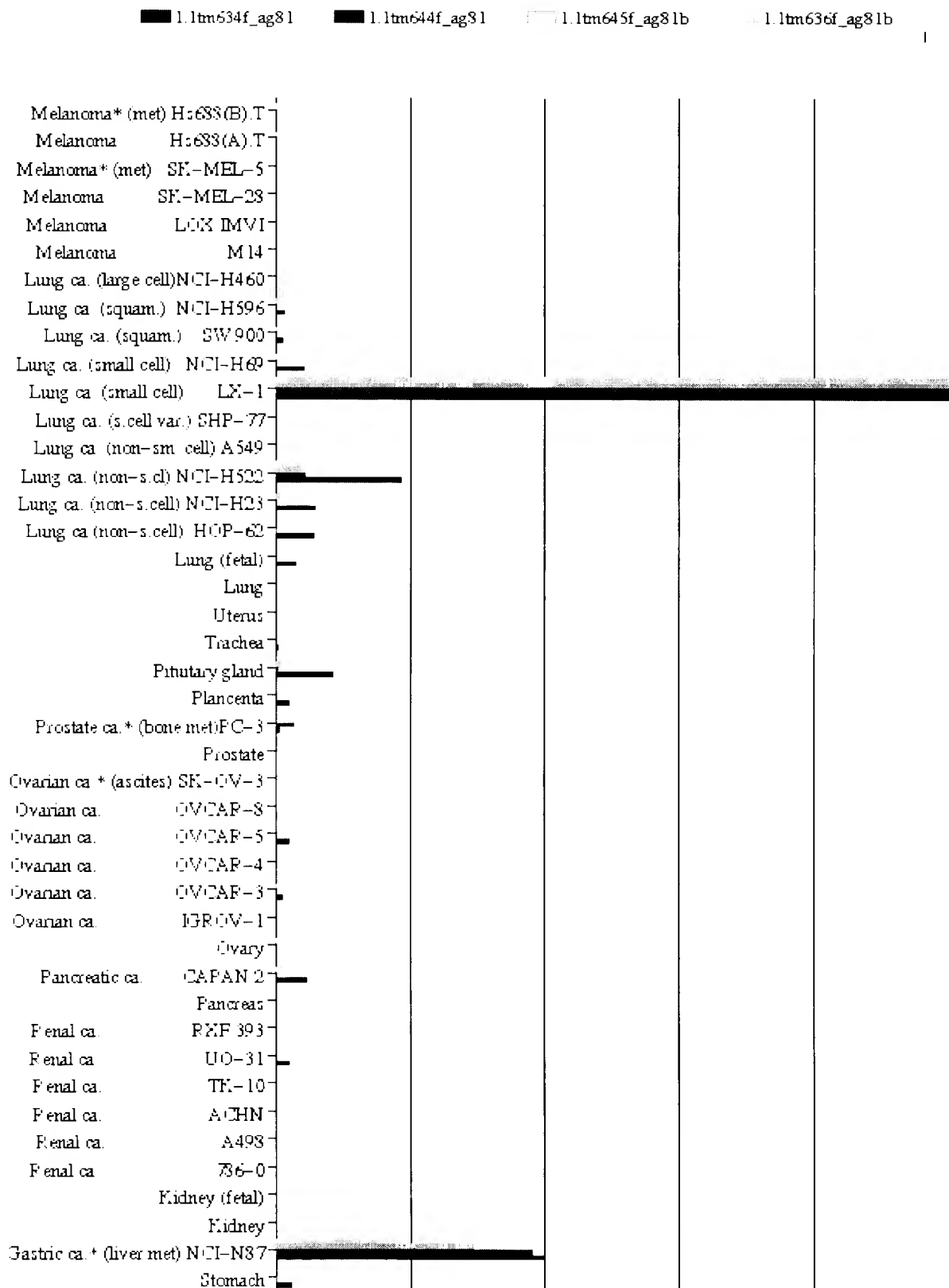


Figure 15, Panel B.

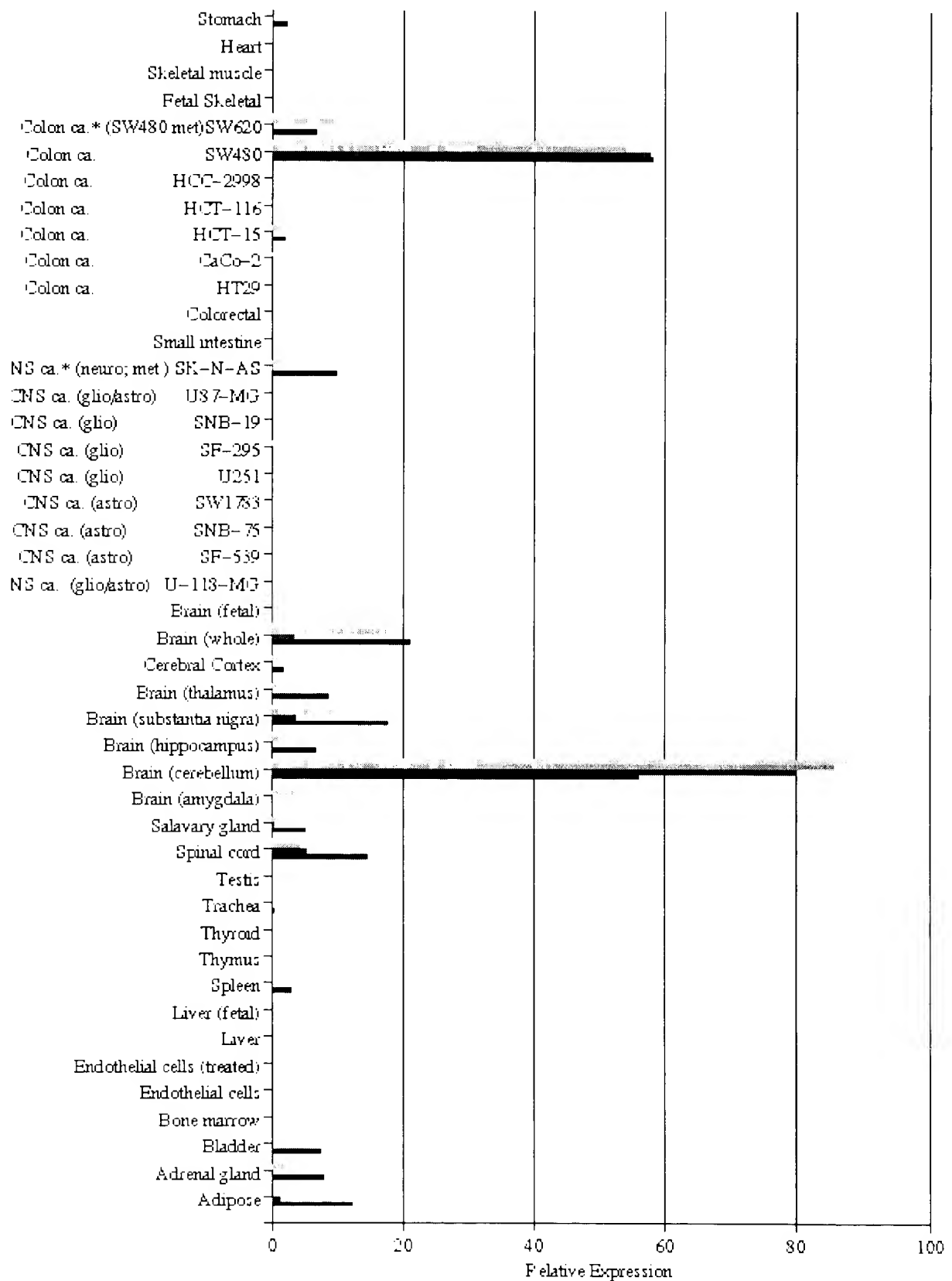


Figure 15, Panel C.

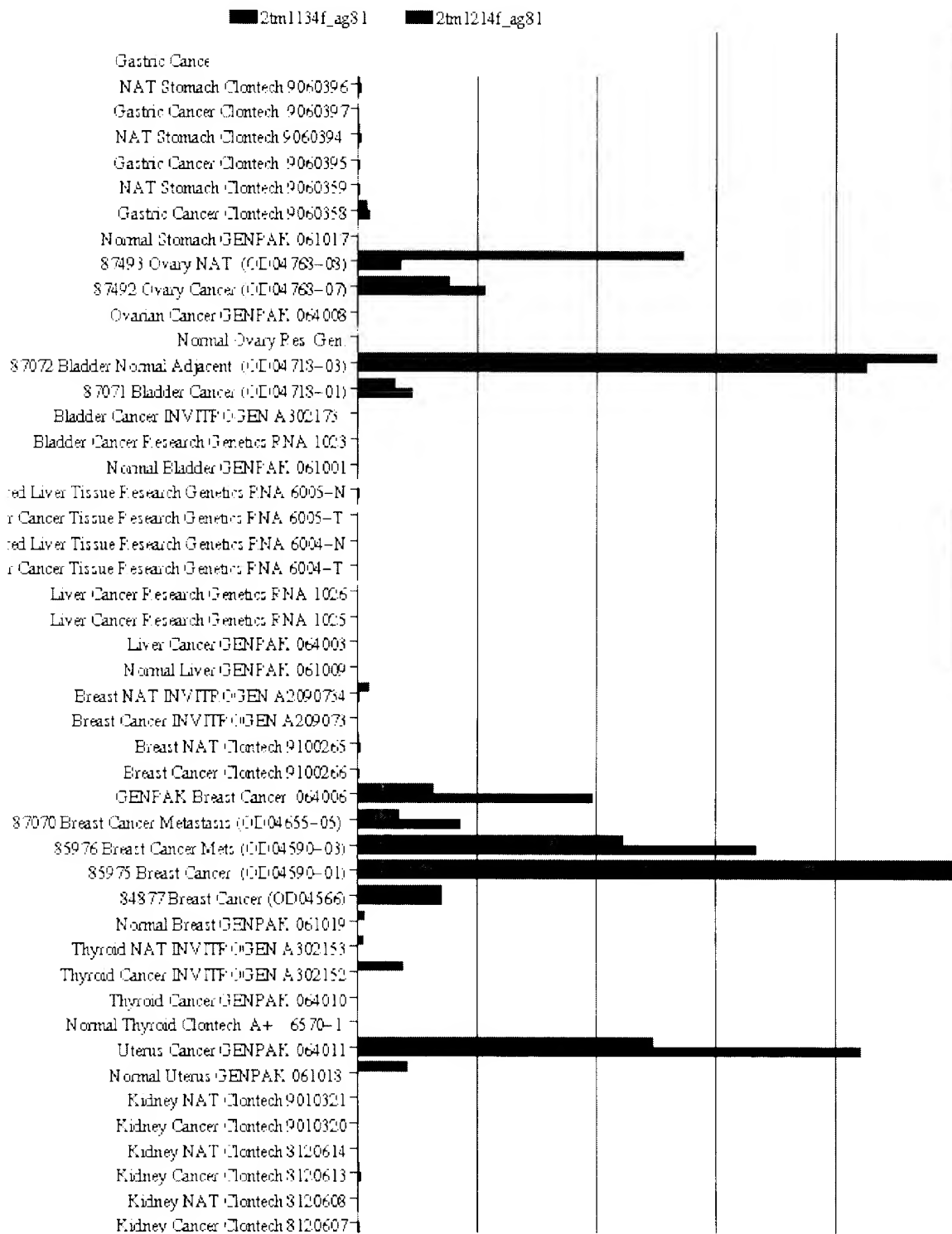


Figure 15, Panel D.

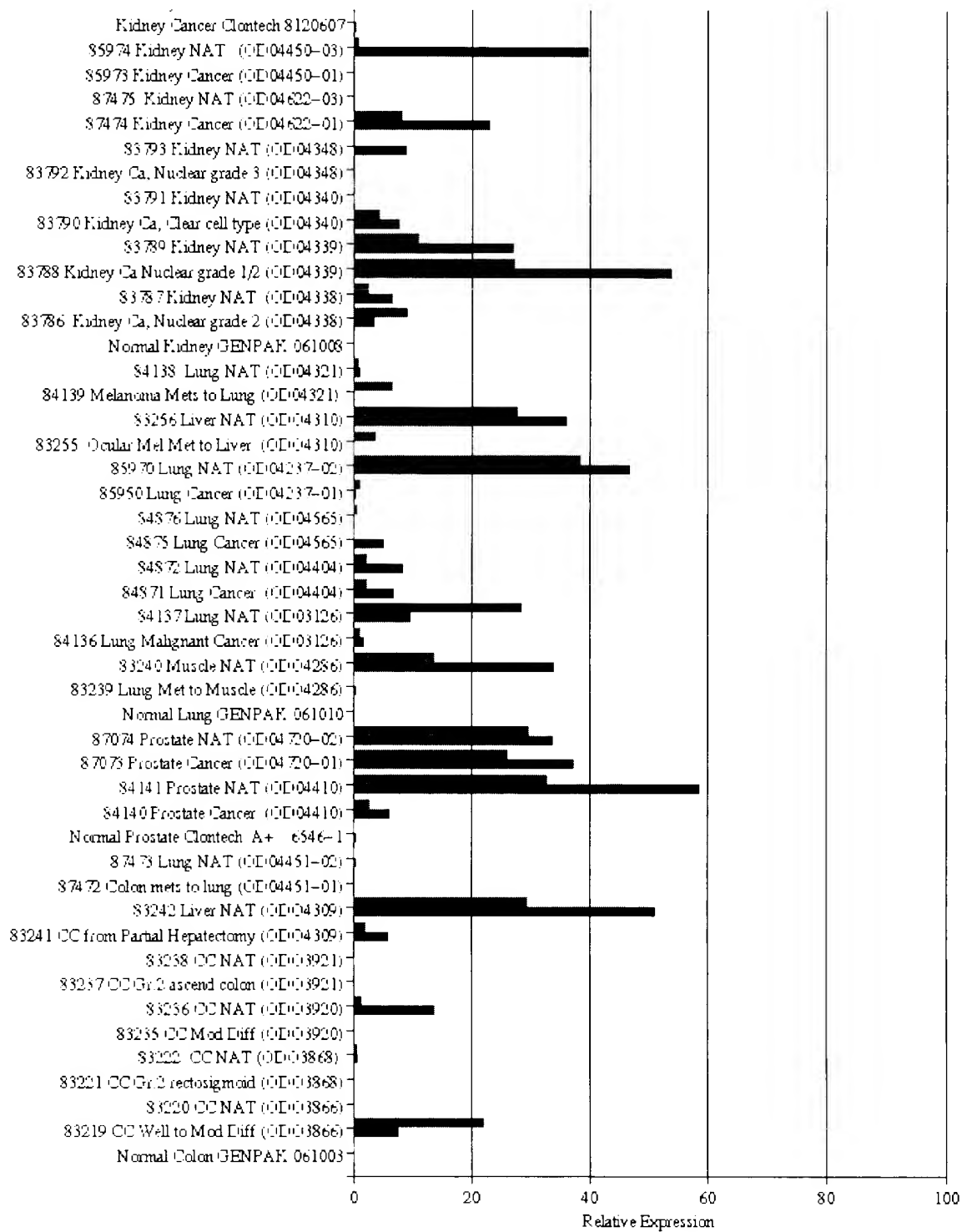


FIGURE 16.

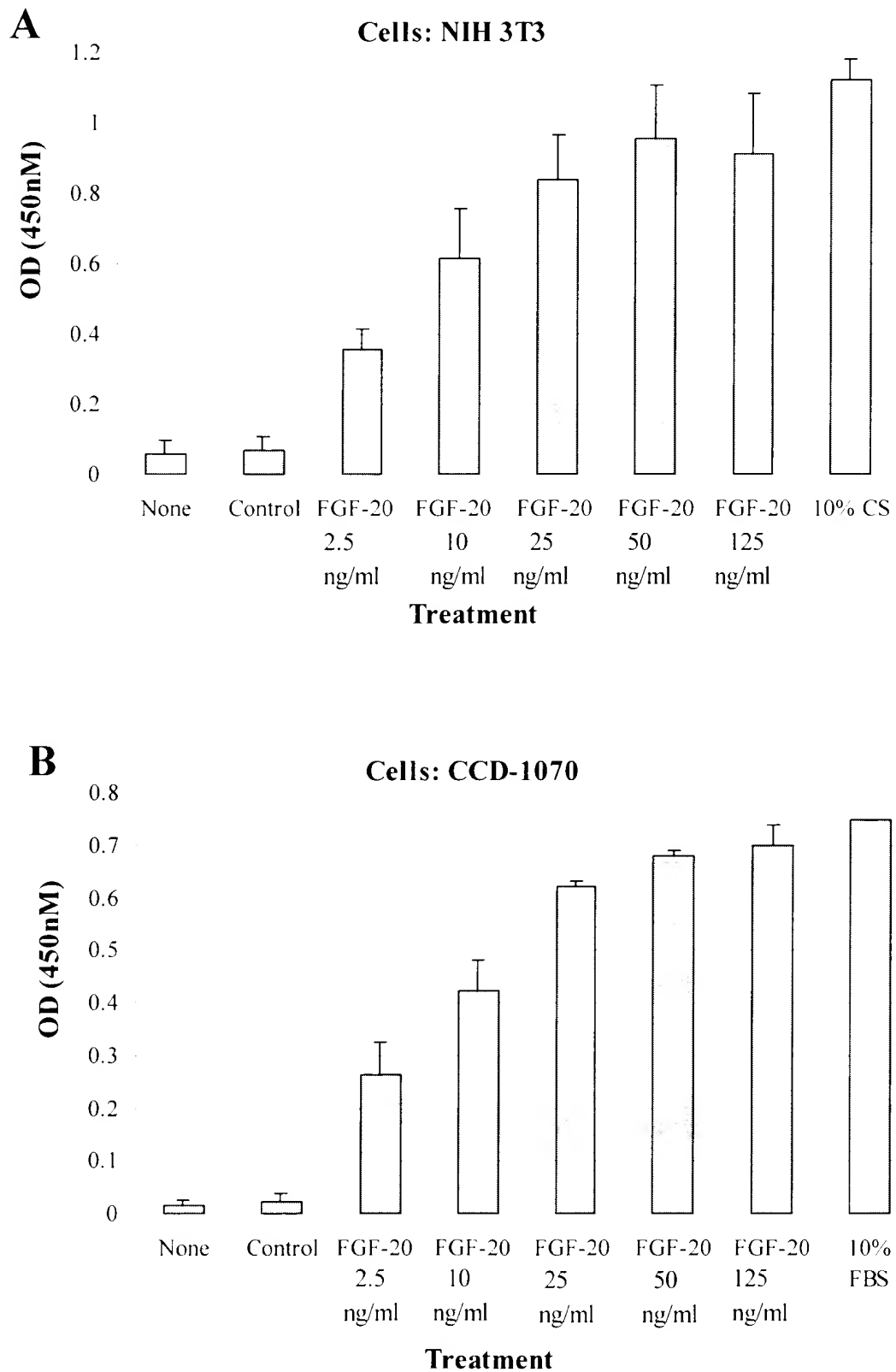


FIGURE 16 (continued).

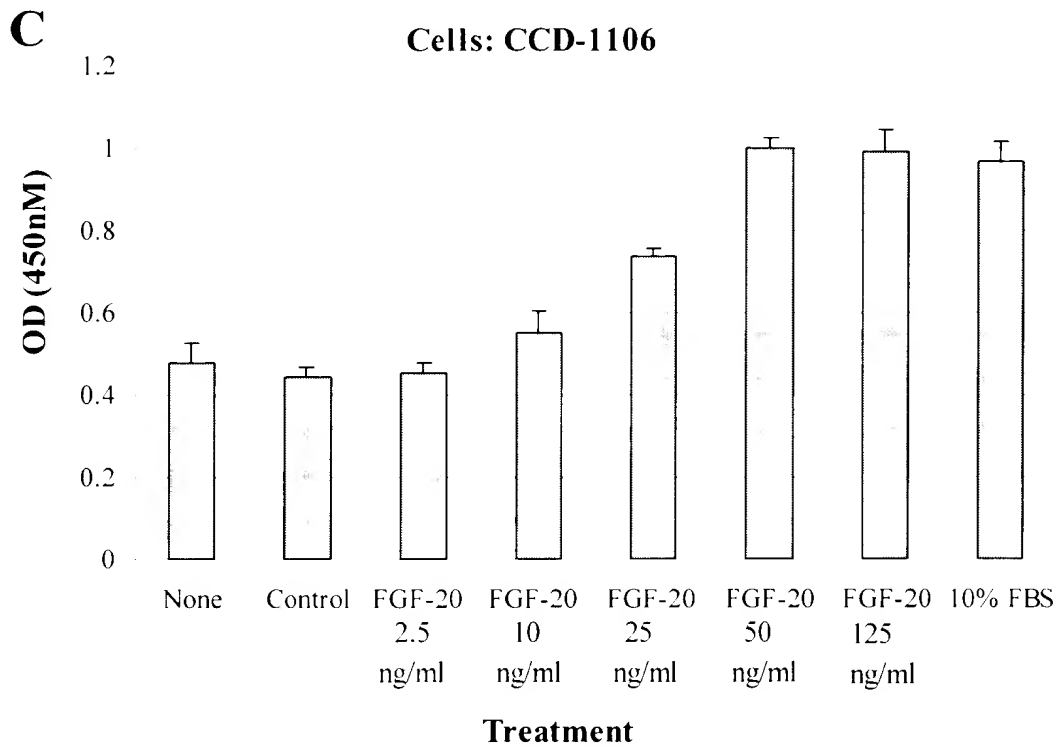


FIGURE 17.

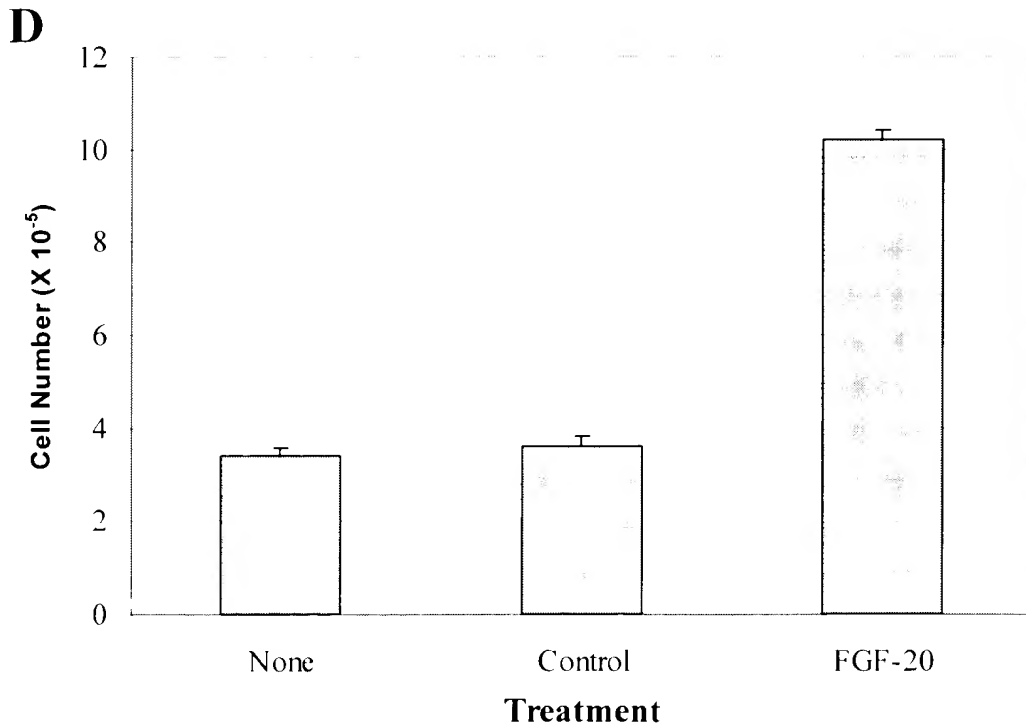


FIGURE 18.

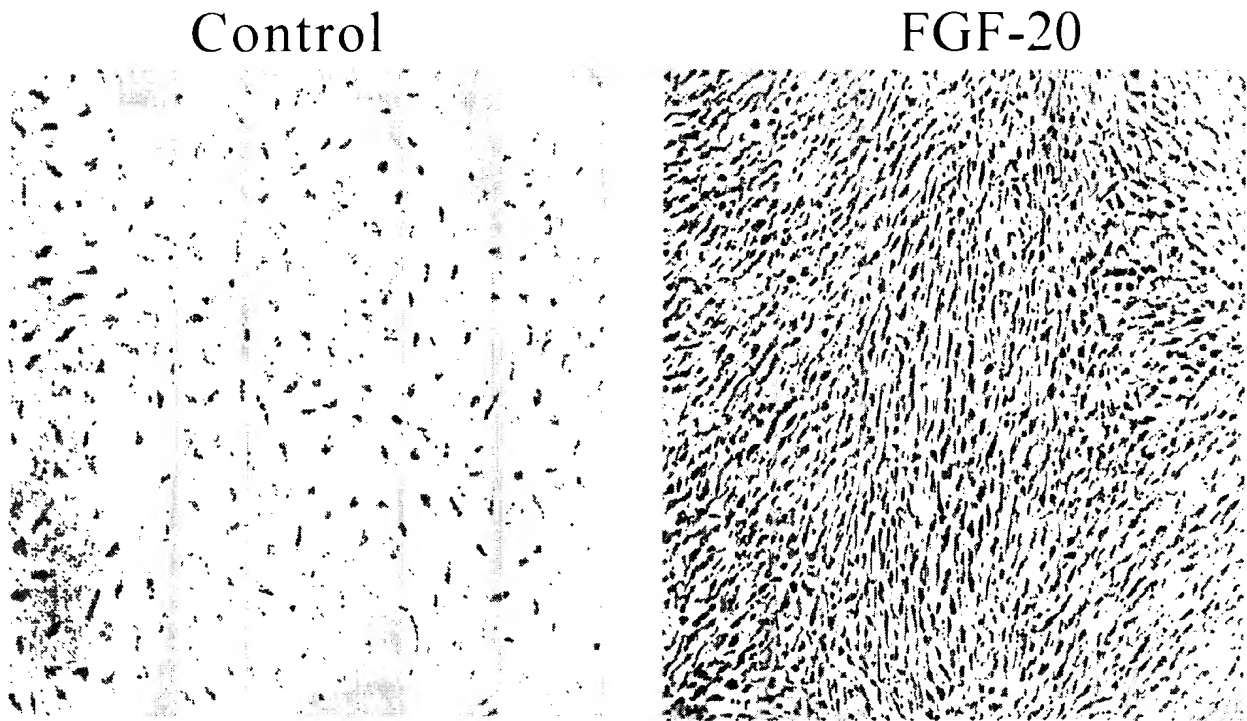


FIGURE 19.

TRADOCS.1

